

sequence_listing.ST25
SEQUENCE LISTING

<110> Karolinska Innovations AB

Ingelman-Sundberg, Magnus

Karlgren, Maria

Gomez, Alvin

<120> Drug target in cancer therapy

<130> P05980PC00/HAM/em

<150> SE0203137-5

<151> 2002-10-24

<150> US 60/420,787

<151> 2002-10-24

<160> 10

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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<221> Primer

<222> (1)..(27)

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27

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28

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Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg
35 40 45

Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly
50 55 60

Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr
65 70 75 80

Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu
85 90 95

Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly
100 105 110

Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe
115 120 125

Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala
130 135 140

Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly
145 150 155 160

Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser
165 170 175

Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp
180 185 190

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Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu
195 200 205

Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly
210 215 220

Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val
225 230 235 240

Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys
245 250 255

Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly
260 265 270

Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala
275 280 285

Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr
290 295 300

Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly
305 310 315 320

Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro
325 330 335

Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His
340 345 350

Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr
355 360 365

Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro
370 375 380

Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln
385 390 395 400

Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His
405 410 415

Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val
420 425 430

Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala
435 440 445

Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro
450 455 460

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<211> 2432

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tcaccagcca cgtcctc atg gcc ctg ctc ttg ctg ttc ctg ggc ctc 170
Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu
1 5 10
ctg ggg ctc tgg ggg ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca 218
Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro
15 20 25
gct gcc cggtggccc ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac 266
Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn
30 35 40
ctg cac ttg ctg cgt ctg tcg caa cag gac ccg tcc ctg atg gag ctc 314
Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu
45 50 55
tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag 362
Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys
60 65 70 75
acg gtg gtg ctg acg ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc 410
Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly
80 85 90
ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc 458
Sida 6

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95								100							105

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Ile	Gln	Arg	Gly	Gly	Gly	Ile	Phe	Phe	Ser	Ser	Gly	Ala	Arg	Trp	Arg	
110						115					120					
gct	gcc	cgc	cag	tcc	acg	gtg	cgt	gcc	ctg	cac	agc	ctg	gcc	gtg	ggc	554
Ala	Ala	Arg	Gln	Phe	Thr	Val	Arg	Ala	Leu	His	Ser	Leu	Gly	Val	Gly	
125						130				135						
cgg	gag	ccg	gtg	gct	gac	aag	att	ctg	cag	gag	ctg	aaa	tgc	ctc	tct	602
Arg	Glu	Pro	Val	Ala	Asp	Lys	Ile	Leu	Gln	Glu	Leu	Lys	Cys	Leu	Ser	
140					145				150				155			
ggg	cag	ctg	gat	ggc	tac	aga	ggc	cgg	ccc	ttc	ccg	ctg	gcc	cta	ctg	650
Gly	Gln	Leu	Asp	Gly	Tyr	Arg	Gly	Arg	Pro	Phe	Pro	Leu	Ala	Leu	Leu	
160						165						170				
ggc	tgg	gct	ccc	tcc	aat	atc	acc	ttc	gcg	ctc	ctc	ttc	ggc	cgc	cga	698
Gly	Trp	Ala	Pro	Ser	Asn	Ile	Thr	Phe	Ala	Leu	Leu	Phe	Gly	Arg	Arg	
175							180					185				
ttt	gac	tac	cg	gac	ccc	gtg	ttt	gtg	tcc	ctg	ctg	ggt	ctc	atc	gat	746
Phe	Asp	Tyr	Arg	Asp	Pro	Val	Phe	Val	Ser	Leu	Leu	Gly	Leu	Ile	Asp	
190							195					200				
gag	gtc	atg	gtc	ctc	ttg	ggg	tcc	cct	ggc	ctg	cag	ctg	ttc	aac	gtc	794
Glu	Val	Met	Val	Leu	Leu	Gly	Ser	Pro	Gly	Leu	Gln	Leu	Phe	Asn	Val	
205						210					215					
tac	cca	tgg	ctc	ggg	gcc	ctg	ctc	cag	ctg	cac	cgg	ccc	gtc	ctg	cgc	842
Tyr	Pro	Trp	Leu	Gly	Ala	Leu	Leu	Gln	Leu	His	Arg	Pro	Val	Leu	Arg	
220					225					230					235	
aag	atc	gag	gag	gtc	cgt	gcc	att	ctg	agg	acc	ctc	ctg	gag	gcg	cgg	890
Lys	Ile	Glu	Glu	Val	Arg	Ala	Ile	Leu	Arg	Thr	Leu	Leu	Glu	Ala	Arg	
240						245							250			
agg	ccc	cac	gtg	tgc	ccg	ggg	gac	ccc	gtg	tgc	agc	tat	gtg	gac	gcc	938
Arg	Pro	His	Val	Cys	Pro	Gly	Asp	Pro	Val	Cys	Ser	Tyr	Val	Asp	Ala	
255						260						265				
ctg	atc	cag	cag	gga	cag	ggg	gat	gac	ccc	gag	ggc	ctg	ttt	gct	gag	986
Leu	Ile	Gln	Gln	Gly	Gln	Gly	Asp	Asp	Pro	Glu	Gly	Leu	Phe	Ala	Glu	
270						275						280				
gcc	aac	gcg	gtg	gcc	tgc	acc	ctg	gac	atg	gtc	atg	gcc	ggg	acg	gag	1034
Ala	Asn	Ala	Val	Ala	Cys	Thr	Leu	Asp	Met	Val	Met	Ala	Gly	Thr	Glu	
285						290					295					
acg	acc	tcg	gcc	acg	ctg	cag	tgg	gcc	gca	ctt	ctg	atg	ggc	cgg	cac	1082
Thr	Thr	Ser	Ala	Thr	Leu	Gln	Trp	Ala	Ala	Leu	Leu	Met	Gly	Arg	His	
300					305					310					315	
ccg	gac	gtg	cag	ggc	cgg	gtg	cag	gag	gag	cta	gac	cgc	gtg	ctg	ggc	1130
Pro	Asp	Val	Gln	Gly	Arg	Val	Gln	Glu	Glu	Leu	Asp	Arg	Val	Leu	Gly	
320							325						330			
cct	ggg	cgg	act	ccc	cg	ctg	gag	gac	cag	cag	gct	ctg	ccc	tac	aca	1178
Pro	Gly	Arg	Thr	Pro	Arg	Leu	Glu	Asp	Gln	Gln	Ala	Leu	Pro	Tyr	Thr	
335							340						345			
agc	gcc	gtg	ctc	cac	gag	gtg	cag	cgg	tcc	atc	acg	ctc	ctg	ccg	cac	1226
Ser	Ala	Val	Leu	His	Glu	Val	Gln	Arg	Phe	Ile	Thr	Leu	Leu	Pro	His	
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Pro Lys Gly Thr Pro Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp		
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Glu Thr Gln Trp Gln Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu		
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Asp Ala Asn Gly His Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser		
415 420 425		
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Ala Gly Arg Arg Val Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu		
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Phe Leu Leu Phe Ala Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro		
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Pro Gly Val Ser Pro Ala Ser Leu Asp Thr Thr Pro Ala Arg Ala Phe		
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Thr Met Arg Pro Arg Ala Gln Ala Leu Cys Ala Val Pro Arg Pro		
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tcaccagcca cgtcctc 137